

1633

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RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/377,675A  
 DATE: 07/05/2000  
 TIME: 12:26:05

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C--> 11 <110> APPLICANT: Olwin, Bradley B.  
 12 <120> TITLE OF INVENTION: CHIMERIC FIBROBLAST GROWTH FACTOR PROTEINS, NUCLEIC  
 13 <130> FILE REFERENCE: 2848-32  
 14 <140> CURRENT APPLICATION NUMBER: US/09/377,675A  
 15 <150> CURRENT FILING DATE: 1999-08-19  
 16 <160> PRIOR APPLICATION NUMBER: 60/097,160  
 17 <170> PRIOR FILING DATE: 1998-08-19  
 18 <180> NUMBER OF SEQ ID NOS: 27  
 19 <190> SOFTWARE: PatentIn Ver. 2.0  
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 21 <210> LENGTH: 556  
 22 <220> TYPE: DNA  
 23 <230> ORGANISM: chimeric sequence  
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 26 <260> LOCATION: (8)..(553)  
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 33 1 5 10  
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 35 tgg aaa aag gcg gct gct ggt tct atc act acc ctg cca gct ctg cca 97  
 36 Trp Lys Lys Ala Ala Ala Gly Ser Ile Thr Thr Leu Pro Ala Leu Pro  
 37 15 20 25 30  
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 39 gaa gac ggt ggt tct ggt gcc ttc cca cca ggt cac ttc aaa gac cca 145  
 40 Glu Asp Gly Gly Ser Gly Ala Phe Pro Pro Gly His Phe Lys Asp Pro  
 41 35 40 45  
 42  
 43 aaa cgt ctg tac tgc aaa aac ggt ggt ttc ttc ctg cgc atc cac ccc 193  
 44 Lys Arg Leu Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile His Pro  
 45 50 55 60  
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 47 gac ggc cga gtg gac ggg gtc cgc gag aag agc gac cca cac atc aaa 241  
 48 Asp Gly Arg Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile Lys  
 49 65 70 75  
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 51 cta caa ctt caa gca gaa gag aga ggg gtt gtg tct atc aaa gga gtg 289  
 52 Leu Gln Leu Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val  
 53 80 85 90  
 54  
 55 tgt gca aac cgt tac ctt gct atg aaa gaa gat gga aga tta cta gct 337  
 56 Cys Ala Asn Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala  
 57 95 100 105 110  
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 59 tct aaa tgt gtt aca gac gag tgt ttc ttt ttt gaa cga ttg gag tct 385  
 60 Ser Lys Cys Val Thr Asp Glu Cys Phe Phe Phe Glu Arg Leu Glu Ser  
 61 115 120 125  
 62  
 63 aat aac tac aat act tac cgg tca agg aaa tac acc agt tgg tat gtg 433  
 64 Asn Asn Tyr Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val  
 65 130 135 140  
 66  
 67 gca ctg aaa cga act ggg cag tat aaa ctt gga tcc aaa aca gga cct 481

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68 Ala Leu Lys Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro
69      145      150      155
71 ggg cag aaa gct ata ctt ttt cca atg tct gct aag agc gaa cag 529
72 Gly Gln Lys Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser Glu Gln
73      160      165      170
75 aaa ctc atc tct gaa gag gat ctg tga 556
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83 <213> ORGANISM: chimeric sequence
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89 Lys Ala Ala Ala Gly Ser Ile Thr Thr Leu Pro Ala Leu Pro Glu Asp
90      20      25      30
92 Gly Gly Ser Gly Ala Phe Pro Pro Gly His Phe Lys Asp Pro Lys Arg
93      35      40      45
95 Leu Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile His Pro Asp Gly
96      50      55      60
98 Arg Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile Lys Leu Gln
99      65      70      75      80
101 Leu Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val Cys Ala
102      85      90      95
104 Asn Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser Lys
105      100      105      110
107 Cys Val Thr Asp Glu Cys Phe Phe Phe Glu Arg Leu Glu Ser Asn Asn
108      115      120      125
110 Tyr Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val Ala Leu
111      130      135      140
113 Lys Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly Gln
114      145      150      155      160
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119 Ile Ser Glu Glu Asp Leu
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128 <220> FEATURE:
129 <221> NAME/KEY: CDS
130 <222> LOCATION: (11)..(553)
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135      1      5      10
137 cag gaa ttc gcg gct gct ggt tct atc act acc ctg cca gct ctg cca 97

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138 Gln Glu Phe Ala Ala Ala Gly Ser Ile Thr Thr Leu Pro Ala Leu Pro
139      15      20      25
141 gaa gac ggt ggt tct ggt gcc ttc cca cca ggt cac ttc aaa gac cca 145
142 Glu Asp Gly Gly Ser Gly Ala Phe Pro Pro Gly His Phe Lys Asp Pro
143 30      35      40      45
145 aaa cgt ctg tac tgc aaa aac ggt ggt ttc ttc ctg cgc atc cac ccc 193
146 Lys Arg Leu Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile His Pro
147      50      55      60
149 gac ggc cga gtg gac ggg gtc cgc gag aag agc gac cca cac atc aaa 241
150 Asp Gly Arg Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile Lys
151      65      70      75
153 cta caa ctt caa gca gaa gag aga ggg gtt gtg tct atc aaa gga gtg 289
154 Leu Gln Leu Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val
155      80      85      90
157 tgt gca aac cgt tac ctt gct atg aaa gaa gat gga aga tta cta gct 337
158 Cys Ala Asn Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala
159      95      100      105
161 tct aaa tgt gtt aca gac gag tgt ttc ttt ttt gaa cga ttg gag tct 385
162 Ser Lys Cys Val Thr Asp Glu Cys Phe Phe Phe Glu Arg Leu Glu Ser
163 110      115      120      125
165 aat aac tac aat act tac cgg tca agg aaa tac acc agt tgg tat gtg 433
166 Asn Asn Tyr Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val
167      130      135      140
169 gca ctg aaa cga act ggg cag tat aaa ctt gga tcc aaa aca gga cct 481
170 Ala Leu Lys Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro
171      145      150      155
173 ggg cag aaa gct ata ctt ttt ctt cca atg tct gct aag agc gaa cag 529
174 Gly Gln Lys Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser Glu Gln
175      160      165      170
177 aaa ctc atc tct gaa gag gat ctg tga 556
178 Lys Leu Ile Ser Glu Glu Asp Leu
179      175      180
182 <210> SEQ ID NO: 4
183 <211> LENGTH: 181
184 <212> TYPE: PRT
185 <213> ORGANISM: chimeric sequence
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191 Ala Ala Ala Gly Ser Ile Thr Thr Leu Pro Ala Leu Pro Glu Asp Gly
192      20      25      30
194 Gly Ser Gly Ala Phe Pro Pro Gly His Phe Lys Asp Pro Lys Arg Leu
195      35      40      45
197 Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile His Pro Asp Gly Arg
198      50      55      60
200 Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile Lys Leu Gln Leu
201      65      70      75      80
203 Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val Cys Ala Asn
204      85      90      95

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206 Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser Lys Cys
207      100      105      110
209 Val Thr Asp Glu Cys Phe Phe Phe Glu Arg Leu Glu Ser Asn Asn Tyr
210      115      120      125
212 Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val Ala Leu Lys
213      130      135      140
215 Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly Gln Lys
216 145      150      155      160
218 Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser Glu Gln Lys Leu Ile
219      165      170      175
221 Ser Glu Glu Asp Leu
222      180
225 <210> SEQ ID NO: 5
226 <211> LENGTH: 146
227 <212> TYPE: PRT
228 <213> ORGANISM: Bos taurus
230 <400> SEQUENCE: 5
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234 Phe Lys Asp Pro Lys Arg Leu Tyr Cys Lys Asn Gly Gly Phe Phe Leu
235      20      25      30
237 Arg Ile His Pro Asp Gly Arg Val Asp Gly Val Arg Glu Lys Ser Asp
238      35      40      45
240 Pro His Ile Lys Leu Gln Leu Gln Ala Glu Glu Arg Gly Val Val Ser
241      50      55      60
243 Ile Lys Gly Val Cys Ala Asn Arg Tyr Leu Ala Met Lys Glu Asp Gly
244 65      70      75      80
246 Arg Leu Leu Ala Ser Lys Cys Val Thr Asp Glu Cys Phe Phe Phe Glu
247      85      90      95
249 Arg Leu Glu Ser Asn Asn Tyr Asn Thr Tyr Arg Ser Arg Lys Tyr Ser
250      100      105      110
252 Ser Trp Tyr Val Ala Leu Lys Arg Thr Gly Gln Tyr Lys Leu Gly Pro
253      115      120      125
255 Lys Thr Gly Pro Gly Gln Lys Ala Ile Leu Phe Leu Pro Met Ser Ala
256 130      135      140
258 Lys Ser
259 145
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263 <211> LENGTH: 146
264 <212> TYPE: PRT
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267 <400> SEQUENCE: 6
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272      20      25      30
274 Arg Ile His Pro Asp Gly Arg Val Asp Gly Val Arg Glu Lys Ser Asp
275      35      40      45
277 Pro His Ile Lys Leu Gln Leu Gln Ala Glu Glu Arg Gly Val Val Ser

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278      50      55      60
280 Ile Lys Gly Val Cys Ala Asn Arg Tyr Leu Ala Met Lys Glu Asp Gly
281 65      70      75      80
283 Arg Leu Leu Ala Ser Lys Cys Val Thr Asp Glu Cys Phe Phe Phe Glu
284      85      90      95
286 Arg Leu Glu Ser Asn Asn Tyr Asn Thr Tyr Arg Ser Arg Lys Tyr Thr
287      100      105      110
289 Ser Trp Tyr Val Ala Leu Lys Arg Thr Gly Gln Tyr Lys Leu Gly Ser
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293      130      135      140
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296 145
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300 <211> LENGTH: 140
301 <212> TYPE: PRT
302 <213> ORGANISM: Bos taurus
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309      20      25      30
311 Gly Thr Lys Asp Arg Ser Asp Gly His Ile Gln Leu Phe Leu Cys Ala
312      35      40      45
314 Glu Ser Ile Gly Glu Val Tyr Ile Lys Ser Thr Glu Thr Gly Gln Phe
315      50      55      60
317 Leu Ala Met Asp Thr Asp Gly Leu Leu Tyr Gly Ser Gln Thr Pro Asp
318 65      70      75      80
320 Glu Glu Cys Leu Phe Leu Glu Arg Leu Glu Glu Asn His Tyr Asn Thr
321      85      90      95
323 Tyr Ile Ser Lys Lys His Ala Glu Lys His Trp Phe Val Gly Leu Lys
324      100      105      110
326 Lys Asn Gly Arg Ser Lys Leu Glu Pro Arg Thr His Phe Gly Gln Lys
327      115      120      125
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330      130      135      140
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334 <211> LENGTH: 140
335 <212> TYPE: PRT
336 <213> ORGANISM: Homo sapiens
338 <400> SEQUENCE: 8
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343      20      25      30
345 Gly Thr Arg Asp Arg Ser Asp Gln His Ile Gln Leu Gln Leu Ser Ala
346      35      40      45
348 Glu Ser Tyr Gly Glu Tyr Tyr Ile Lys Ser Thr Glu Thr Gly Gln Tyr
349      50      55      60

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VERIFICATION SUMMARY                      DATE: 07/05/2000  
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